RAW SEQUENCE LISTING
ERROR REPORT

BIO. 'TNOLOGY
S.._rEMS.
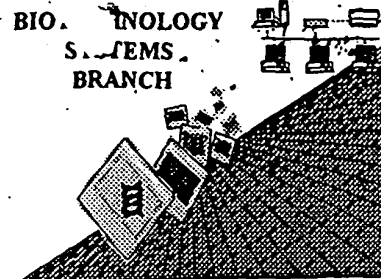BRANCH

#12

The Biotechnology Systems Branch of the Scientific and Technical Information
Center (STIC) detected errors when processing the following computer readable
form:

Application Serial Number: _US 09/479,608_

Source: _OIPE_

Date Processed by STIC: _08 09 2001_

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE
   APPLICANT, WITH A NOTICE TO COMPLY or,
2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A
   NOTICE TO COMPLY
FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.
PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)
PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE <u>CHECKER
VERSION 3.0 PROGRAM</u>, ACCESSIBLE THROUGH THE U.S. PATENT AND
TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program
employing a logical and intuitive user-interface to check whether a sequence listing is in
compliance with format and content rules. Checker Version 3.0 works for sequence listings
generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old
rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual
Property Organization (WIPO) Standard ST.25.
Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-
compliant. Checker allows public users to check sequence listings in Computer Readable form
(CRF) before submitting them to the United States Patent and Trademark Office (USPTO).
Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence
listings, thus saving time and money.

<u>Checker Version 3.0 can be down loaded from the USPTO website at the following address:</u>
http://www.uspto.gov/web/offices/pac/checker

ERROR DETECTED	SUGGESTED CORRECTION	SERIAL NUMBER: 09/479'608

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFT

1 _____ Wrapped Nucleics
     Wrapped Aminos

The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."

2 _____ Invalid Line Length

The rules require that a line not exceed 72 characters in length. This includes white spaces.

3 _____ Misaligned Amino
     Numbering

The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.

4 _____ Non-ASCII

The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.

5 _____ Variable Length

Sequence(s) _____ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.

6 _____ PatentIn 2.0
     "bug"

A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.

7 _____ Skipped Sequences
     (OLD RULES)

Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i)   SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.

8 _____ Skipped Sequences
     (NEW RULES)

Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence.
<210> sequence id number
<400> sequence id number
000

9 _____ Use of n's or Xaa's
     (NEW RULES)

Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

10 _____ Invalid <213>
     Response

Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence

11 _✓_ Use of <220>

Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32)   (Sec. 1.823 of Sequence Rules)

12 _____ PatentIn 2.0
     "bug"

Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

13 _____ Misuse of n

n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.

AMC/MH – Biotechnology Systems Branch – 08/21/2001

The types of errors shown exist <u>throughout</u> the Sequence Listing. Please check subsequent sequences for similar errors.

RAW SEQUENCE LISTING   DATE: 08/09/2001
PATENT APPLICATION: US/09/479,608   TIME: 13:18:12

Input Set : A:\35918.txt
Output Set: N:\CRF3\08092001\I479608.raw

```
 5 <110> APPLICANT: Drmanac, R.
 6       Drmanac, S.
 7       Kita, D.                                    Does Not Comply
 8       Cooke, C.                           Corrected Diskette Needed
 9       Xu, C.
11 <120> TITLE OF INVENTION: ENHANCED SEQUENCING BY HYBRIDIZATION USING POOLS OF PROBES
13 <130> FILE REFERENCE: 28110/35918
15 <140> CURRENT APPLICATION NUMBER: US 09/479,608
16 <141> CURRENT FILING DATE: 2000-01-06
18 <150> PRIOR APPLICATION NUMBER: US 60/115,284
19 <151> PRIOR FILING DATE: 1999-01-06
21 <160> NUMBER OF SEQ ID NOS: 71
23 <170> SOFTWARE: PatentIn version 3.0
25 <210> SEQ ID NO: 1
26 <211> LENGTH: 10
27 <212> TYPE: DNA
28 <213> ORGANISM: Artificial Sequence
30 <220> FEATURE:
31 <223> OTHER INFORMATION:    Description required in field 223
33 <400> SEQUENCE: 1
34 aaaaaaaaaa                                                      10
37 <210> SEQ ID NO: 2
38 <211> LENGTH: 10
39 <212> TYPE: DNA
40 <213> ORGANISM: Artificial Sequence
42 <220> FEATURE:
43 <223> OTHER INFORMATION:   Description of artificial sequence required
45 <400> SEQUENCE: 2
46 acacacacac                                                      10
48 <210> SEQ ID NO: 3
49 <211> LENGTH: 20
50 <212> TYPE: DNA
51 <213> ORGANISM: Artificial Sequence
53 <220> FEATURE:
54 <223> OTHER INFORMATION:   description of artificial sequence required
56 <400> SEQUENCE: 3
57 atctgtgtct gaagtagtcc                                           20
59 <210> SEQ ID NO: 4
60 <211> LENGTH: 20
61 <212> TYPE: DNA
62 <213> ORGANISM: Artificial Sequence
64 <220> FEATURE:
65 <223> OTHER INFORMATION: _____
67 <400> SEQUENCE: 4
68 atctctggct gaagtagtcc                                           20
70 <210> SEQ ID NO: 5
71 <211> LENGTH: 43
```

The types of errors shown exist _throughout_ the Sequence Listing. Please check subsequent sequences for similar errors.

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72 <212> TYPE: DNA
73 <213> ORGANISM: Artificial Sequence
75 <220> FEATURE:
76 <221> NAME/KEY: misc_feature
77 <222> LOCATION:
78 <223> OTHER INFORMATION: b = C or G or T
80 <400> SEQUENCE: 5
81 bbbbbbattt cbbbbbgcac tbbbbgtttg bbbacacgbb bbb
83 <210> SEQ ID NO: 6
84 <211> LENGTH: 43
85 <212> TYPE: DNA
86 <213> ORGANISM: Artificial Sequence
88 <220> FEATURE:
89 <221> NAME/KEY: misc_feature
90 <222> LOCATION:
91 <223> OTHER INFORMATION: b = C or G or T
93 <400> SEQUENCE: 6
94 bbbbbbattt gbbbacactb bbbgtttcbb bbbgcacgbb bbb                43
96 <210> SEQ ID NO: 7
97 <211> LENGTH: 10
98 <212> TYPE: DNA
99 <213> ORGANISM: Artificial Sequence
101 <220> FEATURE:
102 <223> OTHER INFORMATION:
104 <400> SEQUENCE: 7
105 ggtctcccca                                                    10
107 <210> SEQ ID NO: 8
108 <211> LENGTH: 10
109 <212> TYPE: DNA
110 <213> ORGANISM: Artificial Sequence
112 <220> FEATURE:
113 <223> OTHER INFORMATION:
115 <400> SEQUENCE: 8
116 gtctccccaa                                                    10
118 <210> SEQ ID NO: 9
119 <211> LENGTH: 10
120 <212> TYPE: DNA
121 <213> ORGANISM: Artificial Sequence
124 <220> FEATURE:
125 <223> OTHER INFORMATION:
127 <400> SEQUENCE: 9
128 tctccccaag                                                    10
130 <210> SEQ ID NO: 10
131 <211> LENGTH: 10
132 <212> TYPE: DNA
133 <213> ORGANISM: Artificial Sequence
135 <220> FEATURE:
136 <223> OTHER INFORMATION:
138 <400> SEQUENCE: 10
```

— Field 223 with description of artificial sequence required

```
139 ctccccaagg                                              10
141 <210> SEQ ID NO: 11
142 <211> LENGTH: 10
143 <212> TYPE: DNA
144 <213> ORGANISM: Artificial Sequence
146 <220> FEATURE:
147 <223> OTHER INFORMATION:
149 <400> SEQUENCE: 11
150 tccccaaggc                                              10
152 <210> SEQ ID NO: 12
153 <211> LENGTH: 10
154 <212> TYPE: DNA
155 <213> ORGANISM: Artificial Sequence
157 <220> FEATURE:
158 <223> OTHER INFORMATION:
160 <400> SEQUENCE: 12
161 ccccaaggcg                                              10
163 <210> SEQ ID NO: 13
164 <211> LENGTH: 10
165 <212> TYPE: DNA
166 <213> ORGANISM: Artificial Sequence
168 <220> FEATURE:
169 <223> OTHER INFORMATION:
171 <400> SEQUENCE: 13
172 cccaaggcgc                                              10
174 <210> SEQ ID NO: 14
175 <211> LENGTH: 10
176 <212> TYPE: DNA
177 <213> ORGANISM: Artificial Sequence
179 <220> FEATURE:
180 <223> OTHER INFORMATION:
182 <400> SEQUENCE: 14
183 ccaaggcgca                                              10
185 <210> SEQ ID NO: 15
186 <211> LENGTH: 10
187 <212> TYPE: DNA
188 <213> ORGANISM: Artificial Sequence
190 <220> FEATURE:
191 <223> OTHER INFORMATION:
193 <400> SEQUENCE: 15
194 caaggcgcac                                              10
197 <210> SEQ ID NO: 16
198 <211> LENGTH: 30
199 <212> TYPE: DNA
200 <213> ORGANISM: Artificial sequence
202 <220> FEATURE:
203 <223> OTHER INFORMATION:
205 <400> SEQUENCE: 16
206 tgcttgccac aggtctcccc aaggcgcact                        30
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Field 223 description required (handwritten annotation)

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/479,608

DATE: 08/09/2001
TIME: 13:18:12

Input Set : A:\35918.txt
Output Set: N:\CRF3\08092001\I479608.raw

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210 <211> LENGTH: 10
211 <212> TYPE: DNA
212 <213> ORGANISM: Artificial Sequence
214 <220> FEATURE:
215 <223> OTHER INFORMATION:
217 <400> SEQUENCE: 17
218 aggtctcccc                                                  10
221 <210> SEQ ID NO: 18
222 <211> LENGTH: 10
223 <212> TYPE: DNA
224 <213> ORGANISM: Artificial Sequence
226 <220> FEATURE:
227 <223> OTHER INFORMATION:
229 <400> SEQUENCE: 18
230 ggtctcccca                                                  10
233 <210> SEQ ID NO: 19
234 <211> LENGTH: 10
235 <212> TYPE: DNA
236 <213> ORGANISM: Artificial Sequence
238 <220> FEATURE:
239 <223> OTHER INFORMATION:
241 <400> SEQUENCE: 19
242 gtctccccaa                                                  10
244 <210> SEQ ID NO: 20
245 <211> LENGTH: 10
246 <212> TYPE: DNA
247 <213> ORGANISM: Artificial Sequence
249 <220> FEATURE:
250 <223> OTHER INFORMATION:
252 <400> SEQUENCE: 20
253 tctccccaag                                                  10
255 <210> SEQ ID NO: 21
256 <211> LENGTH: 10
257 <212> TYPE: DNA
258 <213> ORGANISM: Artificial Sequence
260 <220> FEATURE:
261 <223> OTHER INFORMATION:
263 <400> SEQUENCE: 21
264 ctccccaagg                                                  10
266 <210> SEQ ID NO: 22
267 <211> LENGTH: 10
268 <212> TYPE: DNA
269 <213> ORGANISM: Artificial Sequence
271 <220> FEATURE:
272 <223> OTHER INFORMATION:
274 <400> SEQUENCE: 22
275 tccccaaggc                                                  10
277 <210> SEQ ID NO: 23
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```
278 <211> LENGTH: 10
279 <212> TYPE: DNA
280 <213> ORGANISM: Artificial Sequence
282 <220> FEATURE:
283 <223> OTHER INFORMATION:
285 <400> SEQUENCE: 23
286 ccccaaggcg                                                    10
288 <210> SEQ ID NO: 24
289 <211> LENGTH: 10
290 <212> TYPE: DNA
291 <213> ORGANISM: Artificial Sequence
293 <220> FEATURE:
294 <223> OTHER INFORMATION:
296 <400> SEQUENCE: 24
297 cccaaggcgc                                                    10
299 <210> SEQ ID NO: 25
300 <211> LENGTH: 10
301 <212> TYPE: DNA
302 <213> ORGANISM: Artificial Sequences
304 <220> FEATURE:
305 <223> OTHER INFORMATION:
308 <400> SEQUENCE: 25
309 ccaaggcgca                                                    10
311 <210> SEQ ID NO: 26
312 <211> LENGTH: 10
313 <212> TYPE: DNA
314 <213> ORGANISM: Artificial Sequence
316 <220> FEATURE:
317 <223> OTHER INFORMATION:
319 <400> SEQUENCE: 26
320 caaggcgcac                                                    10
322 <210> SEQ ID NO: 27
323 <211> LENGTH: 10
324 <212> TYPE: DNA
325 <213> ORGANISM: Artificial Sequence
327 <220> FEATURE:
328 <223> OTHER INFORMATION:
330 <400> SEQUENCE: 27
331 caggtctccc                                                    10
333 <210> SEQ ID NO: 28
334 <211> LENGTH: 10
335 <212> TYPE: DNA
336 <213> ORGANISM: Artificial Sequences
338 <220> FEATURE:
339 <223> OTHER INFORMATION:
341 <400> SEQUENCE: 28
342 gcttgccaca                                                    10
344 <210> SEQ ID NO: 29
345 <211> LENGTH: 10
```

Input Set : **A:\35918.txt**
Output Set: **N:\CRF3\08092001\I479608.raw**

NOTICE TO COMPLY WITH REQUIREMENTS FOR PATENT APPLICATIONS CONTAINING NUCLEOTIDE SEQUENCE AND/OR AMINO ACID SEQUENCE DISCLOSURES

The nucleotide and/or amino acid sequence disclosure contained in this application does not comply with the requirements for such a disclosure as set forth in 37 CFR 1.821 - 1.825 for the following reason(s):

[X] 1. This application clearly fails to comply with the requirements of 37 CFR 1.821-1.825. Applicant's attention is directed to these regulations, published at 114 OG 29, May 15, 1990 and at 55 FR 18230, May 1, 1990.

[X] 2. This application does not contain, as a separate part of the disclosure on paper copy, a "Sequence Listing" as required by 37 CFR 1.821(c).

[X] 3. A copy of the "Sequence Listing" in computer readable form has not been submitted as required by 37 CFR 1.821(e).

[ ] 4. A copy of the "Sequence Listing" in computer readable form has been submitted. However, the content of the computer readable form does not comply with the requirements of 37 CFR 1.822 and/or 1.823, as indicated on the attached copy of the marked-up "Raw Sequence Listing."

[ ] 5. The computer readable form that has been filed with this application has been found to be damaged and/or unreadable as indicated on the attached CRF Diskette Problem Report. A substitute computer readable form must be submitted as required by 37 CFR 1.825(d).

[ ] 6. The paper copy of the "Sequence Listing" is not the same as the computer readable form of the "Sequence Listing" as required by 37 CFR 1.821(e).

[ ] 7. Other: ———————————————————————————————————

Applicant must provide:

[X] An initial or substitute computer readable form (CRF) copy of the "Sequence Listing"

[X] An initial or substitute paper copy of the "Sequence Listing", as well as an amendment directing its entry into the specification

[X] A statement that the content of the paper and computer readable copies are the same and, where applicable, include no new matter, as required by 37 CFR 1.821(e) or 1.821(f) or 1.821(g) or 1.825(b) or 1.825(d)

For questions regarding compliance with these requirements, please contact

For Rules Interpretation, call (703) 308-1123
For CRF submission help, call (703) 308-4212
For PatentIn software help, call (703) 557-0400

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